SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung
ALGENETECH

<120> Gene involved in the biosynthesis of carotenoid and marine microorganism, paracoccus haeundaesis, producing the carotenoid

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35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn
65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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35 40 45

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
50 55 60

Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
65 70 75 80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val

85 90 95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
100 105 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
115 120 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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35 40 45

Asp Pro Asp Leu Ser Pro His Trp Leu Ala Arg Leu Lys Pro Leu Arg
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Arg Ala Asn Trp Pro Asp Gln Glu Val Arg Phe Pro Arg His Ala Arg
65 70 75 80

Arg Leu Ala Thr Gly Tyr Gly Ser Leu Asp Gly Ala Ala Leu Ala Asp
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Ala Val Ala Arg Ser Gly Ala Glu Ile Arg Trp Asn Ser Asp Ile Ala
100 105 110

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115 120 125

Ala Gly Ala Val Leu Asp Gly Arg Gly Ala Gln Pro Ser Arg His Leu
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Pro His Gly Val Pro Arg Pro Met Ile Met Asp Ala Thr Val Thr Gln
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Gln Asp Gly Tyr Arg Phe Ile Tyr Leu Leu Pro Phe Ser Pro Thr Arg
180 185 190

Ile Leu Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asn Leu Asp Asp
195 200 205

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Thr Gly Ala Glu Val Arg Arg Glu Arg Gly Ile Leu Pro Ile Ala Leu

225 230 235 240

Ala His Asp Ala Ala Gly Phe Trp Ala Asp His Ala Glu Gly Pro Val
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Leu Pro Tyr Ala Ala Gln Val Ala Asp Val Val Ala Gly Leu Ser Gly
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Pro Pro Gly Thr Asp Ala Leu Arg Gly Ala Ile Arg Asp Tyr Ala Ile
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Asp Arg Ala Arg Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu
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Asn Ala
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ctggccctgg ccatccgcct gcagtccgcg ggcatcgcca ccaccctggt cgaggcccgg 120

gacaagcccg gcgggcgcgc ctatgtctgg cacgatcagg gccatgtctt cgacgcgggc 180

ccgaccgtca tcaccgaccc cgatgcgctc aaggagctgt gggcgctgac cgggcaggac 240

atggcgcgcg acgtgacgct gatgccggtg tcgcccttct atcgactgat gtggccgggc 300

gggaaggtct tcgattacgt gaacgaggcc gatcagctgg agcgccagat cgcccagttc 360

aacccggacg acctggaagg ataccgccgc ttccgtgatt acgcggagga ggtgtatcag 420

gagggctacg tcaagctggg caccgtgccc ttcctcaagc tgggccagat gctcaaggcc 480

gcgcccgcgc tgatgaagct ggaggcctat aagtccgtcc atgccaaggt cgcgaccttc 540

atcaaggacc cctatctgcg gcaggcgttt tcgtatcaca cgctgctggt gggcgggaat 600

cccttctcga ccagctcgat ctatgcgctg atccacgcgc tggagcggcg cggcggggtc 660

tggttcgcca agggcggcac caaccagctg gtcgcgggca tggtcgcgct gttcgaacgg 720

cttggcggcc agatgatgct gaacgccaag gtcgcccgga tcgagaccga gggcgcgcgg 780

accacgggcg tcaccctggc ggacgggcgg tctttaaggg ccgacatggt cgccagcaac 840

ggcgacgtca tgcacaacta tcgcgacctg ctgggccaca cggcccgcgg gcagagccgc 900

gcgaaatcgc tggaccgcaa gcgctggtcc atgtcgttgt tcgtgctgca tttcggtctg 960

cgcgaggcgc ccaaggacat cgcgcatcac accatcctgt tcggcccccg ctacagggag 1020

ctggtcaacg agatcttcaa gggcccgaag ctggccgagg atttctcgct gtacctgcat 1080

tcgccctgca cgaccgatcc ggacatggcg cctccgggca tgtccacgca ttacgtgctg 1140

gcccccgtgc cgcatctggg ccgcgccgag atcgattggg cggtcgaggg gccgcgctat 1200

gccgaccgca tcctggcgtc cctggaggag cggctgatcc cgaacctgcg cgccaacctg 1260

accacgacgc gcatcttcac gcccgccgat ttcgccagcg aactgaacgc ccatcacggc 1320

agcgccttct cggtcgagcc gatcctgacg caatccgcgt ggttccggcc gcacaaccgc 1380

gacaagacga tccgcaactt ctatctggtc ggcgcgggca cccatccggg cgcgggcatt 1440

ccgggcgtcg tgggctcggc caaggccacg gcccaggtga tgctgtccga cctggcgggc 1500

gcatga 1506

<210> 12
<211> 501
<212> PRT
<213> crtI amino acid

<400> 12

Met Asn Ala His Ser Pro Ala Ala Lys Thr Ala Ile Val Ile Gly Ala
1 5 10 15

Gly Phe Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ser Ala Gly Ile
20 25 30

Ala Thr Thr Leu Val Glu Ala Arg Asp Lys Pro Gly Gly Arg Ala Tyr
35 40 45

Val Trp His Asp Gln Gly His Val Phe Asp Ala Gly Pro Thr Val Ile
50 55 60

Thr Asp Pro Asp Ala Leu Lys Glu Leu Trp Ala Leu Thr Gly Gln Asp
65 70 75 80

Met Ala Arg Asp Val Thr Leu Met Pro Val Ser Pro Phe Tyr Arg Leu

85 90 95

Met Trp Pro Gly Gly Lys Val Phe Asp Tyr Val Asn Glu Ala Asp Gln
100 105 110

Leu Glu Arg Gln Ile Ala Gln Phe Asn Pro Asp Asp Leu Glu Gly Tyr
115 120 125

Arg Arg Phe Arg Asp Tyr Ala Glu Glu Val Tyr Gln Glu Gly Tyr Val
130 135 140

Lys Leu Gly Thr Val Pro Phe Leu Lys Leu Gly Gln Met Leu Lys Ala
145 150 155 160

Ala Pro Ala Leu Met Lys Leu Glu Ala Tyr Lys Ser Val His Ala Lys
165 170 175

Val Ala Thr Phe Ile Lys Asp Pro Tyr Leu Arg Gln Ala Phe Ser Tyr
180 185 190

His Thr Leu Leu Val Gly Gly Asn Pro Phe Ser Thr Ser Ser Ile Tyr
195 200 205

Ala Leu Ile His Ala Leu Glu Arg Arg Gly Gly Val Trp Phe Ala Lys
210 215 220

Gly Gly Thr Asn Gln Leu Val Ala Gly Met Val Ala Leu Phe Glu Arg
225 230 235 240

Leu Gly Gly Gln Met Met Leu Asn Ala Lys Val Ala Arg Ile Glu Thr
245 250 255

Glu Gly Ala Arg Thr Thr Gly Val Thr Leu Ala Asp Gly Arg Ser Leu
260 265 270

Arg Ala Asp Met Val Ala Ser Asn Gly Asp Val Met His Asn Tyr Arg
275 280 285

Asp Leu Leu Gly His Thr Ala Arg Gly Gln Ser Arg Ala Lys Ser Leu
290 295 300

Asp Arg Lys Arg Trp Ser Met Ser Leu Phe Val Leu His Phe Gly Leu
305 310 315 320

Arg Glu Ala Pro Lys Asp Ile Ala His His Thr Ile Leu Phe Gly Pro
325 330 335

Arg Tyr Arg Glu Leu Val Asn Glu Ile Phe Lys Gly Pro Lys Leu Ala
340 345 350

Glu Asp Phe Ser Leu Tyr Leu His Ser Pro Cys Thr Thr Asp Pro Asp
355 360 365

Met Ala Pro Pro Gly Met Ser Thr His Tyr Val Leu Ala Pro Val Pro
370 375 380

His Leu Gly Arg Ala Glu Ile Asp Trp Ala Val Glu Gly Pro Arg Tyr

385 390 395 400

Ala Asp Arg Ile Leu Ala Ser Leu Glu Glu Arg Leu Ile Pro Asn Leu
405 410 415

Arg Ala Asn Leu Thr Thr Thr Arg Ile Phe Thr Pro Ala Asp Phe Ala
420 425 430

Ser Glu Leu Asn Ala His His Gly Ser Ala Phe Ser Val Glu Pro Ile
435 440 445

Leu Thr Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile
450 455 460

Arg Asn Phe Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile
465 470 475 480

Pro Gly Val Val Gly Ser Ala Lys Ala Thr Ala Gln Val Met Leu Ser
485 490 495

Asp Leu Ala Gly Ala
500

<210> 13
<211> 915
<212> DNA
<213> crtB gene

<400> 13
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acggcggcca agctgatgcc gccgggcatc cgcgacgaca cggtgatgct ctatgcctgg 120

tgccgccacg cggatgacgt gatcgacggt caggccctgg gcagccgccc cgaggcggtg 180

aacgacccgc aggcgcggct ggacggcctg cgcgtcgaca cgctggcggc cctgcagggc 240

gacggtccgg tgaccccgcc ctttgccgcg ctgcgcgcgg tggcgcggcg gcatgatttc 300

ccgcaggcct ggcccatgga cctgatcgaa ggcttcgcga tggatgtcga ggcgcgcgac 360

tatcgcacgc tggatgacgt gctggaatat cctatcacg tcgcaggcat cgtcggcgtg 420

atgatggccc gcgtgatggg cgtgcgcgac gatcctgtcc tggaccgcgc ctgcgacctg 480

gggctggcgt tccagctgac caacatcgcg cgcgacgtga tcgacgatgc gcgcatcggg 540

cggtgctatc tgccggggga ctggctggac caggcgggcg cgcggatcga cgggccggtg 600

ccgtcgccgg agctgtacac agtgatcctc cggctgttgg atgaggcgga accctattac 660

gcgtcggcgc gggtgggtct ggcggatctg ccaccgcgct gcgcctggtc catcgccgcc 720

gcgctacgga tctatcgcgc catcgggctg cgcatccgca agagcgggcc gcaggcctat 780

cgccagcgga tcagcacgtc caaggctgcc aagatcggcc tgctgggcgt cgggggctgg 840

gatgtcgcgc gatcacgcct gccgggggcg ggcgtgtcgc ggcagggcct ctggacccgg 900

ccgcatcacg tctag 915

<210> 14
<211> 304
<212> PRT
<213> crtB amino acid

<400> 14

Met Ser Asp Leu Val Leu Thr Ser Thr Glu Ala Ile Thr Gln Gly Ser
1 5 10 15

Gln Ser Phe Ala Thr Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Asp
20 25 30

Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile
35 40 45

Asp Gly Gln Ala Leu Gly Ser Arg Pro Glu Ala Val Asn Asp Pro Gln
50 55 60

Ala Arg Leu Asp Gly Leu Arg Val Asp Thr Leu Ala Ala Leu Gln Gly
65 70 75 80

Asp Gly Pro Val Thr Pro Pro Phe Ala Ala Leu Arg Ala Val Ala Arg
85 90 95

Arg His Asp Phe Pro Gln Ala Trp Pro Met Asp Leu Ile Glu Gly Phe
100 105 110

Ala Met Asp Val Glu Ala Arg Asp Tyr Arg Thr Leu Asp Asp Val Leu
115 120 125

Glu Tyr Ser Tyr His Val Ala Gly Ile Val Gly Val Met Met Ala Arg
130 135 140

Val Met Gly Val Arg Asp Asp Pro Val Leu Asp Arg Ala Cys Asp Leu
145 150 155 160

Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp
165 170 175

Ala Arg Ile Gly Arg Cys Tyr Leu Pro Gly Asp Trp Leu Asp Gln Ala
180 185 190

Gly Ala Arg Ile Asp Gly Pro Val Pro Ser Pro Glu Leu Tyr Thr Val
195 200 205

Ile Leu Arg Leu Leu Asp Glu Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
210 215 220

Val Gly Leu Ala Asp Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala
225 230 235 240

Ala Leu Arg Ile Tyr Arg Ala Ile Gly Leu Arg Ile Arg Lys Ser Gly
245 250 255

Pro Gln Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
260 265 270

Gly Leu Leu Gly Val Gly Gly Trp Asp Val Ala Arg Ser Arg Leu Pro
275 280 285

Gly Ala Gly Val Ser Arg Gln Gly Leu Trp Thr Arg Pro His His Val
290 295 300

<210> 15
<211> 882
<212> DNA
<213> crtE gene

<400> 15
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gcccagggat tcggtgccgt gtcgcagccg ctcggcgcgg ccatgagcca tggcgcgctg 120

tcgtcgggca ggcggttccg cggcatgctg atgctgcttg cggcagaggc ctcgggcggg 180

gtctgcgaca cgatcgtcga cgccgcctgc gcggtcgaga tggtgcatgc cgcatcgctg 240

atcttcgacg acctgccctg catggacgat gccgggctgc gccgcggccg gcccgcgacc 300

catgtggcgc atggcgaaag ccgtgccgtg ctgggcggca tcgccctgat caccgaggca 360

atggccctgc tggccggtgc gcgcggcgcg tcgggcacgg tgcgggcgca gctggtgcgg 420

atcctgtcgc ggtccctggg gccgcagggc ctgtgcgccg gccaggacct ggacctgcac 480

gcggccaaga acggcgcggg ggtcgaacag gaacaggacc tgaagaccgg cgtgctgttc 540

atcgccgggc tggagatgct ggccgtgatc aaggagttcg acgccgagga gcagacccag 600

atgatcgact ttggccgtca gctgggccgc gtgttccagt cctatgacga cctgctggac 660

gtcgtgggcg accaggcggc gcttggcaag ataccggtc gcgatgccgc ggcccccggc 720

ccgcggcgcg gccttctggc cgtgtcagac ctgcagaacg tgtcccgtca ttacgaggcc 780

agccgcgccc aactggacgc gatgctgcgc agcaagcgcc ttcaggctcc ggaaatcgcg 840

gccctgctgg aacgggttct gccctacgcc gcgcgcgcct ag 882

<210> 16
<211> 293
<212> PRT
<213> crtE amino acid

<400> 16

Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
1 5 10 15

Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
20 25 30

Ala Ala Met Ser His Gly Ala Leu Ser Ser Gly Arg Arg Phe Arg Gly
35 40 45

Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
50 55 60

Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80

Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly
85 90 95

Arg Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly
100 105 110

Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg
115 120 125

Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg
130 135 140

Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160

Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr
165 170 175

Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu
180 185 190

Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu
195 200 205

Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp
210 215 220

Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly
225 230 235 240

Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg
245 250 255

His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys
260 265 270

Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro
275 280 285

Tyr Ala Ala Arg Ala
290

<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for crt gene

<400> 17
gttccacgac tggggcatc 19

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for crt gene

<400> 18
tccactgacc ttgttggaca aattgccg 28